

SEQUENCE LISTING

049E 1177

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PATENT & TRADEMARK OFFICE

acrosyl synthase

#3

<120> Modification of sucrose synthase gene expression in plant tissue and
uses therefor

<150> 60/251852
<151> 2000-12-08

<170> PatentIn version 3.1

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<210> 1
<211> 2625
<212> DNA
<213> Gossypium hirsutum
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1				5				10						15		
gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca																96
Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser																
			20					25					30			
agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att																144
Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile																
			35				40					45				
cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat																192
Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn																
			50			55					60					
ggt gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg																240
Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu																
65					70				75					80		

cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag	288
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu	
85 90 95	
tac att aga gtg aat gtt cac gcc ctt gtt gtt gag gaa ctc act gtt	336
Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val	
100 105 110	
gct gag tat ctc cac ttc aag gaa gag ctt gtt gat gga agt tca aat	384
Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn	
115 120 125	
gga aac ttt gtt ttg gaa ttg gat ttt gag ccc ttc aac tca tca ttc	432
Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe	
130 135 140	
ccc cgc cca act ctt tca aaa tcc att ggt aat ggt gtg gag ttc cta	480
Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu	
145 150 155 160	
aat cgt cac ctt tgc gca aaa ttg ttc cat gac aag gag agc atg cac	528
Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His	
165 170 175	
cct ttg ctc gaa ttc ctc aga gtc cat tgt cac aag ggc aag aac atg	576
Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met	
180 185 190	
atg ttg aat gac aga att cag aac ttg aat gct ctt caa cat gtt ttg	624
Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu	
195 200 205	
agg aaa gca gag gag tat ctt ggt acc cta cct cct gag aca cca tgt	672
Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys	
210 215 220	
gcc gaa ttc gaa cac cgg ttc cag gaa atc ggt ttg gaa aga ggt tgg	720
Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp	
225 230 235 240	
ggt gac acc gca gaa cgc gtg ctc gag atg atc caa ctc ctt ttg gat	768
Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp	
245 250 255	
ctt ctt gag gca act gat cct tgc acc ctt gag aag ttc ctt ggg aga	816
Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg	
260 265 270	
atc ccc atg gtg ttc aat gtt gtg att ctc act ccc cac gga tac ttc	864
Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe	
275 280 285	

gct caa gac aat gtt ttg ggg tat ccc gac acc ggt ggg cag gtt gtt	912
Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val	
290 295 300	
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Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg	
305 310 315 320	
ata aag caa caa gga ctc aac atc acc cct cga atc ctc att att act	1008
Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr	
325 330 335	
aga ctt ctt cct gat gct gtc gga aca aca tgc ggt caa cga ctt gag	1056
Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu	
340 345 350	
aaa gta tac gga aca gag cac tcg gat att ctt cga gta ccc ttc aga	1104
Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg	
355 360 365	
aca gaa aag gga att gtt cga aaa tgg atc tca aga ttt gaa aaa gtc	1152
Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val	
370 375 380	
tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc	1200
Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser	
385 390 395 400	
aaa gag ttg cac ggc acg cca gat ctg atc atc gga aac nac agc gac	1248
Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp	
405 410 415	
ggc aat atc gtc gcc tcc ttg ctc gca cat aaa tta ggt gtc aca cag	1296
Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln	
420 425 430	
tgc acc atc gcc cat gct ttg gag aag aca aaa tat cca gat tca gat	1344
Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp	
435 440 445	
atc tat tgg aag aag ctt gaa gac aaa tac cat ttc tct tgc caa ttt	1392
Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe	
450 455 460	
aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt	1440
Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser	
465 470 475 480	
act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag	1488
Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu	
485 490 495	

agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt	1536
Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly	
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atc gat gtg ttt gat ccc aaa ttc aac att gtt tcc cct ggt gct gat	1584
Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp	
515 520 525	
atg gag ata tac ttc cct tac acc gaa gag aag cgg agg ttg aag cat	1632
Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His	
530 535 540	
ttc cat cct gag atc gaa gac ctt ctt tac acc aaa gtt gag aat gaa	1680
Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu	
545 550 555 560	
gaa cac tta tgt gtg ctc aat gac cgc aac aag cca att ctg ttc aca	1728
Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr	
565 570 575	
atg cca agg ctt gat cgt gtc aag aac tta acc gga ctc gtc gag tgg	1776
Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp	
580 585 590	
tgc ggc aag aac cca aag ttg cgt gag ttg gct aac ctc gta gtt gta	1824
Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val	
595 600 605	
ggg ggt gat agg cga aag gaa tct aaa gat ttg gaa gag aag gct gaa	1872
Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu	
610 615 620	
atg aag aaa atg ttt gag ctg atc gac aag tac aac ttg aac ggc caa	1920
Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln	
625 630 635 640	
ttc aga tgg ata tca tct caa atg aac aga atc cga aat gtt gaa ctt	1968
Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu	
645 650 655	
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Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu	
660 665 670	
tat gaa gcc ttt gga ttg aca gtt gtg gag gca atg act tgc ggt ttg	2064
Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu	
675 680 685	
cca aca ttc gca acc tgt aac ggt gga cca gcc gag att att gtc cat	2112
Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His	
690 695 700	

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ggg aaa tct ggt ttc aac att gat cct tac cat ggt gat caa gct gct      2160
Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala
705                      710                      715                      720

gac ata ctc gtc gat ttc ttt gaa aag tgt aag aaa gat cca tct cac      2208
Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His
                      725                      730                      735

tgg gat aag atc tcc caa gga ggc ttg aaa cga ata gag gag aag tat      2256
Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr
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aca tgg aag att tac tcg gag aga cta ttg acc ctg aca gga gtg tat      2304
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr
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gga ttc tgg aag cat gtt tcc aac ctt gaa cgc cgt gag agt cgt cgt      2352
Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg
                      770                      775                      780

tac ctt gag atg ttt tat gct ctt aag tac cgt aag ctg gct gaa tca      2400
Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
785                      790                      795                      800

ggt cca ttg gca gag gag taa att gaa cct gtt aaa taa cat tgg gcc      2448
Val Pro Leu Ala Glu Glu Ile Glu Pro Val Lys His Trp Ala
                      805                      810

ggt ttt tct tgg aga ata ata ttc tgt ttt gta att tca att gga gaa      2496
Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu
815                      820                      825                      830

gct cct ttg tat ttc atc ttg tct ttt cct ttt cct ttt ttc gcc ggc      2544
Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe Phe Ala Gly
                      835                      840                      845

att gtt tga aca tgg ggt tgt gcg ccc gtc aat tcc agt taa ata tgg      2592
Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp
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<213> Gossypium hirsutum

<220>

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<223> The 'Xaa' at location 414 stands for Asn, Asp, His, or Tyr.

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<222> (1240)..(1240)

<223> n = any nucleotide (a,g,c,t)

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Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
35 40 45

Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
50 55 60

Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
65 70 75 80

Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
85 90 95

Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100 105 110

Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
115 120 125

Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
130 135 140

Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
145 150 155 160

Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
165 170 175

Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
180 185 190

Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
210 215 220

Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225 230 235 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
 245 250 255
 Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg
 260 265 270
 Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
 275 280 285
 Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
 290 295 300
 Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg
 305 310 315 320
 Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr
 325 330 335
 Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
 340 345 350
 Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg
 355 360 365
 Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val
 370 375 380
 Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser
 385 390 395 400
 Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp
 405 410 415
 Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln
 420 425 430
 Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp
 435 440 445
 Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe
 450 455 460
 Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser
 465 470 475 480
 Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu
 485 490 495
 Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly
 500 505 510

Ile	Asp	Val	Phe	Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	515	520	525
Met	Glu	Ile	Tyr	Phe	Pro	Tyr	Thr	Glu	Glu	Lys	Arg	Arg	Leu	Lys	His	530	535	540
Phe	His	Pro	Glu	Ile	Glu	Asp	Leu	Leu	Tyr	Thr	Lys	Val	Glu	Asn	Glu	545	550	555
Glu	His	Leu	Cys	Val	Leu	Asn	Asp	Arg	Asn	Lys	Pro	Ile	Leu	Phe	Thr	565	570	575
Met	Pro	Arg	Leu	Asp	Arg	Val	Lys	Asn	Leu	Thr	Gly	Leu	Val	Glu	Trp	580	585	590
Cys	Gly	Lys	Asn	Pro	Lys	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Val	Val	595	600	605
Gly	Gly	Asp	Arg	Arg	Lys	Glu	Ser	Lys	Asp	Leu	Glu	Glu	Lys	Ala	Glu	610	615	620
Met	Lys	Lys	Met	Phe	Glu	Leu	Ile	Asp	Lys	Tyr	Asn	Leu	Asn	Gly	Gln	625	630	635
Phe	Arg	Trp	Ile	Ser	Ser	Gln	Met	Asn	Arg	Ile	Arg	Asn	Val	Glu	Leu	645	650	655
Tyr	Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Leu	660	665	670
Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met	Thr	Cys	Gly	Leu	675	680	685
Pro	Thr	Phe	Ala	Thr	Cys	Asn	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Val	His	690	695	700
Gly	Lys	Ser	Gly	Phe	Asn	Ile	Asp	Pro	Tyr	His	Gly	Asp	Gln	Ala	Ala	705	710	715
Asp	Ile	Leu	Val	Asp	Phe	Phe	Glu	Lys	Cys	Lys	Lys	Asp	Pro	Ser	His	725	730	735
Trp	Asp	Lys	Ile	Ser	Gln	Gly	Gly	Leu	Lys	Arg	Ile	Glu	Glu	Lys	Tyr	740	745	750
Thr	Trp	Lys	Ile	Tyr	Ser	Glu	Arg	Leu	Leu	Thr	Leu	Thr	Gly	Val	Tyr	755	760	765
Gly	Phe	Trp	Lys	His	Val	Ser	Asn	Leu	Glu	Arg	Arg	Glu	Ser	Arg	Arg	770	775	780
Tyr	Leu	Glu	Met	Phe	Tyr	Ala	Leu	Lys	Tyr	Arg	Lys	Leu	Ala	Glu	Ser	785	790	795

Val Pro Leu Ala Glu Glu
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<210> 3
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<212> PRT
<213> Gossypium hirsutum

<220>
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<223> n = any nucleotide (a,g,c,t)

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Ile Glu Pro Val Lys
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<210> 4
<211> 37
<212> PRT
<213> Gossypium hirsutum

<220>

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<223> n = any nucleotide (a,g,c,t)

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Ile Gly Glu Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe
20 25 30

Phe Ala Gly Ile Val
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<210> 5
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<213> Gossypium hirsutum

<220>
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<223> n = any nucleotide (a,g,c,t)

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Thr Trp Gly Cys Ala Pro Val Asn Ser Ser
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<210> 6
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<212> PRT
<213> Gossypium hirsutum

<220>
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Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys
1 5 10